



SEQUENCE LISTING

<110> SAKANO, SEIJI
ITO, AKIRA

<120> DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

<130> KP8447DIV

<140> 09/995,593

<141> 2001-11-29

<150> 09/068,740

<151> 1998-06-18

<150> JP 7-299611

<151> 1995-11-17

<150> JP 7-311811

<151> 1995-11-30

<150> PCT/JP96/03356

<151> 1996-11-15

<160> 48

<170> PatentIn Ver. 2.1

<210> 1

<211> 43

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (2)..(4)

<223> Unknown amino acid

<220>

<221> MOD_RES

<222> (7)..(9)

<223> Unknown amino acid

<220>

<221> MOD_RES

<222> (11)..(13)

<223> Unknown amino acid

<220>

<221> MOD_RES

<222> (20)

<223> Unknown amino acid

<220>

<221> MOD_RES

<222> (24)..(25)

<223> Unknown amino acid

<220>
 <221> MOD_RES
 <222> (27)..(29)
 <223> Unknown amino acid

<220>
 <221> MOD_RES
 <222> (31)..(33)
 <223> Unknown amino acid

<220>
 <221> MOD_RES
 <222> (35)..(36)
 <223> Unknown amino acid

<220>
 <221> MOD_RES
 <222> (39)
 <223> Unknown amino acid

<220>
 <221> MOD_RES
 <222> (41)..(42)
 <223> Unknown amino acid

<400> 1
 Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Arg Pro
 1 5 10 15
 Arg Asx Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly Xaa Xaa
 20 25 30
 Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys
 35 40

<210> 2
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 2
 Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly
 1 5 10 15
 Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly Ala Gly Pro Pro Pro
 20 25 30
 Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala
 35 40 45
 Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro
 50 55 60
 Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp
 65 70 75 80

Ser	Ala	Phe	Ser	Asn	Pro	Ile	Arg	Phe	Pro	Phe	Gly	Phe	Thr	Trp	Pro	
				85					90					95		
Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Leu	His	Thr	Asp	Ser	Pro	Asp	
				100					105					110		
Asp	Leu	Ala	Thr	Glu	Asn	Pro	Glu	Arg	Leu	Ile	Ser	Arg	Leu	Ala	Thr	
				115					120					125		
Gln	Arg	His	Leu	Thr	Val	Gly	Glu	Glu	Thr	Ser	Gln	Asp	Leu	His	Ser	
				130					135					140		
Ser	Gly	Arg	Thr	Asp	Leu	Lys	Tyr	Ser	Tyr	Arg	Phe	Val	Cys	Asp	Glu	
				145					150					155		
His	Tyr	Tyr	Gly	Glu	Gly	Cys	Ser	Val	Phe	Cys	Arg	Pro	Arg	Asp	Asp	
				165					170					175		
Ala	Phe	Gly	His	Phe	Thr	Cys	Gly	Glu	Arg	Gly	Glu	Lys	Val	Cys	Asn	
				180					185					190		
Pro	Gly	Trp	Lys	Gly	Pro	Tyr	Cys									
				195					200							

```
<210> 3
<211> 520
<212> PRT
<213> Homo sapiens
```

<400>	3															
Ser	Gly	Val	Phe	Glu	Leu	Lys	Leu	Gln	Glu	Phe	Val	Asn	Lys	Lys	Gly	
1				5					10					15		
Leu	Leu	Gly	Asn	Arg	Asn	Cys	Cys	Arg	Gly	Gly	Ala	Gly	Pro	Pro	Pro	
			20					25					30			
Cys	Ala	Cys	Arg	Thr	Phe	Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	
		35					40					45				
Ser	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr	Tyr	Gly	Ser	Ala	Val	Thr	Pro	
	50					55					60					
Val	Leu	Gly	Val	Asp	Ser	Phe	Ser	Leu	Pro	Asp	Gly	Gly	Gly	Ala	Asp	
65					70					75					80	
Ser	Ala	Phe	Ser	Asn	Pro	Ile	Arg	Phe	Pro	Phe	Gly	Phe	Thr	Trp	Pro	
				85					90					95		
Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Leu	His	Thr	Asp	Ser	Pro	Asp	
			100					105					110			
Asp	Leu	Ala	Thr	Glu	Asn	Pro	Glu	Arg	Leu	Ile	Ser	Arg	Leu	Ala	Thr	
		115					120					125				
Gln	Arg	His	Leu	Thr	Val	Gly	Glu	Glu	Trp	Ser	Gln	Asp	Leu	His	Ser	
	130					135					140					

Ser	Gly	Arg	Thr	Asp	Leu	Lys	Tyr	Ser	Tyr	Arg	Phe	Val	Cys	Asp	Glu	145	150	155	160
His	Tyr	Tyr	Gly	Glu	Gly	Cys	Ser	Val	Phe	Cys	Arg	Pro	Arg	Asp	Asp	165	170	175	
Ala	Phe	Gly	His	Phe	Thr	Cys	Gly	Glu	Arg	Gly	Glu	Lys	Val	Cys	Asn	180	185	190	
Pro	Gly	Trp	Lys	Gly	Pro	Tyr	Cys	Thr	Glu	Pro	Ile	Cys	Leu	Pro	Gly	195	200	205	
Cys	Asp	Glu	Gln	His	Gly	Phe	Cys	Asp	Lys	Pro	Gly	Glu	Cys	Lys	Cys	210	215	220	
Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu	Cys	Ile	Arg	Tyr	Pro	225	230	235	240
Gly	Cys	Leu	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp	Gln	Cys	Asn	Cys	Gln	245	250	255	
Glu	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp	Leu	Asn	Tyr	Cys	Thr	260	265	270	
His	His	Lys	Pro	Cys	Lys	Asn	Gly	Ala	Thr	Cys	Thr	Asn	Thr	Gly	Gln	275	280	285	
Gly	Ser	Tyr	Thr	Cys	Ser	Cys	Arg	Pro	Gly	Tyr	Thr	Gly	Ala	Thr	Cys	290	295	300	
Glu	Leu	Gly	Ile	Asp	Glu	Cys	Asp	Pro	Ser	Pro	Cys	Lys	Asn	Gly	Gly	305	310	315	320
Ser	Cys	Thr	Asp	Leu	Glu	Asn	Ser	Tyr	Ser	Cys	Thr	Cys	Pro	Pro	Gly	325	330	335	
Phe	Tyr	Gly	Lys	Ile	Cys	Glu	Leu	Ser	Ala	Met	Thr	Cys	Ala	Asp	Gly	340	345	350	
Pro	Cys	Phe	Asn	Gly	Gly	Arg	Cys	Ser	Asp	Ser	Pro	Asp	Gly	Gly	Tyr	355	360	365	
Ser	Cys	Arg	Cys	Pro	Val	Gly	Tyr	Ser	Gly	Phe	Asn	Cys	Glu	Lys	Lys	370	375	380	
Ile	Asp	Tyr	Cys	Ser	Ser	Ser	Pro	Cys	Ser	Asn	Gly	Ala	Lys	Cys	Val	385	390	395	400
Asp	Leu	Gly	Asp	Ala	Tyr	Leu	Cys	Arg	Cys	Gln	Ala	Gly	Phe	Ser	Gly	405	410	415	
Arg	His	Cys	Asp	Asp	Asn	Val	Asp	Asp	Cys	Ala	Ser	Ser	Pro	Cys	Ala	420	425	430	
Asn	Gly	Gly	Thr	Cys	Arg	Asp	Gly	Val	Asn	Asp	Phe	Ser	Cys	Thr	Cys	435	440	445	

Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala Pro Val Ser Arg Cys
 450 455 460

Glu His Ala Pro Cys His Asn Gly Ala Thr Cys His Glu Arg Gly His
 465 470 475 480

Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly Gly Pro Asn Cys Gln
 485 490 495

Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala Val Val Asp Leu Thr
 500 505 510

Glu Lys Leu Glu Gly Gln Gly Gly
 515 520

<210> 4
 <211> 702
 <212> PRT
 <213> Homo sapiens

<400> 4
 Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly
 1 5 10 15

Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly Ala Gly Pro Pro Pro
 20 25 30

Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala
 35 40 45

Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro
 50 55 60

Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp
 65 70 75 80

Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro
 85 90 95

Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp
 100 105 110

Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr
 115 120 125

Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser
 130 135 140

Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu
 145 150 155 160

His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp
 165 170 175

Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn
 180 185 190

Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly	195	200	205
Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys	210	215	220
Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro	225	230	235
Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln	245	250	255
Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr	260	265	270
His His Lys Pro Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln	275	280	285
Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ala Thr Cys	290	295	300
Glu Leu Gly Ile Asp Glu Cys Asp Pro Ser Pro Cys Lys Asn Gly Gly	305	310	315
Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly	325	330	335
Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly	340	345	350
Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser Pro Asp Gly Gly Tyr	355	360	365
Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe Asn Cys Glu Lys Lys	370	375	380
Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val	385	390	395
Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly	405	410	415
Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala	420	425	430
Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp Phe Ser Cys Thr Cys	435	440	445
Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala Pro Val Ser Arg Cys	450	455	460
Glu His Ala Pro Cys His Asn Gly Ala Thr Cys His Glu Arg Gly His	465	470	475
Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly Gly Pro Asn Cys Gln	485	490	495

Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala Val Val Asp Leu Thr
 500 505 510
 Glu Lys Leu Glu Gly Gln Gly Gly Pro Phe Pro Trp Val Ala Val Cys
 515 520 525
 Ala Gly Val Ile Leu Val Leu Met Leu Leu Leu Gly Cys Ala Ala Val
 530 535 540
 Val Val Cys Val Arg Leu Arg Leu Gln Lys His Arg Pro Pro Ala Asp
 545 550 555 560
 Pro Cys Arg Gly Glu Thr Glu Thr Met Asn Asn Leu Ala Asn Cys Gln
 565 570 575
 Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly Ala Thr Gln Ile Lys
 580 585 590
 Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp His Ser Ala Asp Lys
 595 600 605
 Asn Gly Phe Lys Ala Arg Tyr Pro Ala Val Asp Tyr Asn Leu Val Gln
 610 615 620
 Asp Leu Lys Gly Asp Asp Thr Ala Val Arg Asp Ala His Ser Lys Arg
 625 630 635 640
 Asp Thr Lys Cys Gln Pro Gln Gly Ser Ser Gly Glu Glu Lys Gly Thr
 645 650 655
 Pro Thr Thr Leu Arg Gly Gly Glu Ala Ser Glu Arg Lys Arg Pro Asp
 660 665 670
 Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val
 675 680 685
 Ile Ser Glu Glu Lys Asp Glu Cys Val Ile Ala Thr Glu Val
 690 695 700

<210> 5
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 5
 Ser Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly
 1 5 10 15
 Glu Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp
 20 25 30
 Arg Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu
 35 40 45
 Lys Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly
 50 55 60

Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
 65 70 75 80
 Ser Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala
 85 90 95
 Trp Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn
 100 105 110
 Asp Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly
 115 120 125
 Met Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly
 130 135 140
 Val Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr
 145 150 155 160
 Tyr Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe
 165 170 175
 Gly His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly
 180 185 190
 Trp Met Gly Pro Glu Cys
 195

<210> 6

<211> 1036

<212> PRT

<213> Homo sapiens

<400> 6

Ser Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly
 1 5 10 15
 Glu Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp
 20 25 30
 Arg Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu
 35 40 45
 Lys Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly
 50 55 60
 Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
 65 70 75 80
 Ser Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala
 85 90 95
 Trp Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn
 100 105 110
 Asp Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly
 115 120 125

Met	Ile	Asn	Pro	Ser	Arg	Gln	Trp	Gln	Thr	Leu	Lys	Gln	Asn	Thr	Gly	130	135	140
Val	Ala	His	Phe	Glu	Tyr	Gln	Ile	Arg	Val	Thr	Cys	Asp	Asp	Tyr	Tyr	145	150	155
Tyr	Gly	Phe	Gly	Cys	Asn	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Phe	Phe	165	170	175
Gly	His	Tyr	Ala	Cys	Asp	Gln	Asn	Gly	Asn	Lys	Thr	Cys	Met	Glu	Gly	180	185	190
Trp	Met	Gly	Pro	Glu	Cys	Asn	Arg	Ala	Ile	Cys	Arg	Gln	Gly	Cys	Ser	195	200	205
Pro	Lys	His	Gly	Ser	Cys	Lys	Leu	Pro	Gly	Asp	Cys	Arg	Cys	Gln	Tyr	210	215	220
Gly	Trp	Gln	Gly	Leu	Tyr	Cys	Asp	Lys	Cys	Ile	Pro	His	Pro	Gly	Cys	225	230	235
Val	His	Gly	Ile	Cys	Asn	Glu	Pro	Trp	Gln	Cys	Leu	Cys	Glu	Thr	Asn	245	250	255
Trp	Gly	Gly	Gln	Leu	Cys	Asp	Lys	Asp	Leu	Asn	Tyr	Cys	Gly	Thr	His	260	265	270
Gln	Pro	Cys	Leu	Asn	Gly	Gly	Thr	Cys	Ser	Asn	Thr	Gly	Pro	Asp	Lys	275	280	285
Tyr	Gln	Cys	Ser	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	Pro	Asn	Cys	Glu	Ile	290	295	300
Ala	Glu	His	Ala	Cys	Leu	Ser	Asp	Pro	Cys	His	Asn	Arg	Gly	Ser	Cys	305	310	315
Lys	Glu	Thr	Ser	Leu	Gly	Phe	Glu	Cys	Glu	Cys	Ser	Pro	Gly	Trp	Thr	325	330	335
Gly	Pro	Thr	Cys	Ser	Thr	Asn	Ile	Asp	Asp	Cys	Ser	Pro	Asn	Asn	Cys	340	345	350
Ser	His	Gly	Gly	Thr	Cys	Gln	Asp	Leu	Val	Asn	Gly	Phe	Lys	Cys	Val	355	360	365
Cys	Pro	Pro	Gln	Trp	Thr	Gly	Lys	Thr	Cys	Gln	Leu	Asp	Ala	Asn	Glu	370	375	380
Cys	Glu	Ala	Lys	Pro	Cys	Val	Asn	Ala	Lys	Ser	Cys	Lys	Asn	Leu	Ile	385	390	395
Ala	Ser	Tyr	Tyr	Cys	Asp	Cys	Leu	Pro	Gly	Trp	Met	Gly	Gln	Asn	Cys	405	410	415
Asp	Ile	Asn	Ile	Asn	Asp	Cys	Leu	Gly	Gln	Cys	Gln	Asn	Asp	Ala	Ser	420	425	430

Cys	Arg	Asp	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Ile	Cys	Pro	Pro	Gly	Tyr	435	440	445
Ala	Gly	Asp	His	Cys	Glu	Arg	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Asn	Pro	450	455	460
Cys	Leu	Asn	Gly	Gly	His	Cys	Gln	Asn	Glu	Ile	Asn	Arg	Phe	Gln	Cys	465	470	475
Leu	Cys	Pro	Thr	Gly	Phe	Ser	Gly	Asn	Leu	Cys	Gln	Leu	Asp	Ile	Asp	485	490	495
Tyr	Cys	Glu	Pro	Asn	Pro	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Tyr	Asn	Arg	500	505	510
Ala	Ser	Asp	Tyr	Phe	Cys	Lys	Cys	Pro	Glu	Asp	Tyr	Glu	Gly	Lys	Asn	515	520	525
Cys	Ser	His	Leu	Lys	Asp	His	Cys	Arg	Thr	Thr	Pro	Cys	Glu	Val	Ile	530	535	540
Asp	Ser	Cys	Thr	Val	Ala	Met	Ala	Ser	Asn	Asp	Thr	Pro	Glu	Gly	Val	545	550	555
Arg	Tyr	Ile	Ser	Ser	Asn	Val	Cys	Gly	Pro	His	Gly	Lys	Cys	Lys	Ser	565	570	575
Gln	Ser	Gly	Gly	Lys	Phe	Thr	Cys	Asp	Cys	Asn	Lys	Gly	Phe	Thr	Gly	580	585	590
Thr	Tyr	Cys	His	Glu	Asn	Ile	Asn	Asp	Cys	Glu	Ser	Asn	Pro	Cys	Arg	595	600	605
Asn	Gly	Gly	Thr	Cys	Ile	Asp	Gly	Val	Asn	Ser	Tyr	Lys	Cys	Ile	Cys	610	615	620
Ser	Asp	Gly	Trp	Glu	Gly	Ala	Tyr	Cys	Glu	Thr	Asn	Ile	Asn	Asp	Cys	625	630	635
Ser	Gln	Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Arg	Asp	Leu	Val	Asn	645	650	655
Asp	Phe	Tyr	Cys	Asp	Cys	Lys	Asn	Gly	Trp	Lys	Gly	Lys	Thr	Cys	His	660	665	670
Ser	Arg	Asp	Ser	Gln	Cys	Asp	Glu	Ala	Thr	Cys	Asn	Asn	Gly	Gly	Thr	675	680	685
Cys	Tyr	Asp	Glu	Gly	Asp	Ala	Phe	Lys	Cys	Met	Cys	Pro	Gly	Gly	Trp	690	695	700
Glu	Gly	Thr	Thr	Cys	Asn	Ile	Ala	Arg	Asn	Ser	Ser	Cys	Leu	Pro	Asn	705	710	715
Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Val	Val	Asn	Gly	Glu	Ser	Phe	Thr	725	730	735

Cys Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr
 740 745 750
 Asn Asp Cys Ser Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp
 755 760 765
 Gly Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro
 770 775 780
 Asp Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe
 785 790 795 800
 Gly Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro
 805 810 815
 Pro Gly His Ser Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys
 820 825 830
 Ile Thr Met Gly Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp
 835 840 845
 Cys Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val
 850 855 860
 Trp Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys
 865 870 875 880
 Pro Ser Gly Gln Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val
 885 890 895
 His Pro Cys Thr Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro
 900 905 910
 Val Lys Thr Lys Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala
 915 920 925
 Asn Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr
 930 935 940
 Thr Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn
 945 950 955 960
 Val Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser
 965 970 975
 Ala Asn Asn Glu Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp
 980 985 990
 Asp Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val
 995 1000 1005
 Ser Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val
 1010 1015 1020
 Arg Val Gln Arg Arg Pro Leu Lys Asn Arg Thr Asp
 1025 1030 1035

<210> 7
 <211> 1187
 <212> PRT
 <213> Homo sapiens

<400> 7

Ser	Gly	Gln	Phe	Glu	Leu	Glu	Ile	Leu	Ser	Met	Gln	Asn	Val	Asn	Gly	1	5	10	15
Glu	Leu	Gln	Asn	Gly	Asn	Cys	Cys	Gly	Gly	Ala	Arg	Asn	Pro	Gly	Asp	20	25	30	
Arg	Lys	Cys	Thr	Arg	Asp	Glu	Cys	Asp	Thr	Tyr	Phe	Lys	Val	Cys	Leu	35	40	45	
Lys	Glu	Tyr	Gln	Ser	Arg	Val	Thr	Ala	Gly	Gly	Pro	Cys	Ser	Phe	Gly	50	55	60	
Ser	Gly	Ser	Thr	Pro	Val	Ile	Gly	Gly	Asn	Thr	Phe	Asn	Leu	Lys	Ala	65	70	75	80
Ser	Arg	Gly	Asn	Asp	Arg	Asn	Arg	Ile	Val	Leu	Pro	Phe	Ser	Phe	Ala	85	90	95	
Trp	Pro	Arg	Ser	Tyr	Thr	Leu	Leu	Val	Glu	Ala	Trp	Asp	Ser	Ser	Asn	100	105	110	
Asp	Thr	Val	Gln	Pro	Asp	Ser	Ile	Ile	Glu	Lys	Ala	Ser	His	Ser	Gly	115	120	125	
Met	Ile	Asn	Pro	Ser	Arg	Gln	Trp	Gln	Thr	Leu	Lys	Gln	Asn	Thr	Gly	130	135	140	
Val	Ala	His	Phe	Glu	Tyr	Gln	Ile	Arg	Val	Thr	Cys	Asp	Asp	Tyr	Tyr	145	150	155	160
Tyr	Gly	Phe	Gly	Cys	Asn	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Phe	Phe	165	170	175	
Gly	His	Tyr	Ala	Cys	Asp	Gln	Asn	Gly	Asn	Lys	Thr	Cys	Met	Glu	Gly	180	185	190	
Trp	Met	Gly	Pro	Glu	Cys	Asn	Arg	Ala	Ile	Cys	Arg	Gln	Gly	Cys	Ser	195	200	205	
Pro	Lys	His	Gly	Ser	Cys	Lys	Leu	Pro	Gly	Asp	Cys	Arg	Cys	Gln	Tyr	210	215	220	
Gly	Trp	Gln	Gly	Leu	Tyr	Cys	Asp	Lys	Cys	Ile	Pro	His	Pro	Gly	Cys	225	230	235	240
Val	His	Gly	Ile	Cys	Asn	Glu	Pro	Trp	Gln	Cys	Leu	Cys	Glu	Thr	Asn	245	250	255	
Trp	Gly	Gly	Gln	Leu	Cys	Asp	Lys	Asp	Leu	Asn	Tyr	Cys	Gly	Thr	His	260	265	270	

Gln Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys
 275 280 285
 Tyr Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile
 290 295 300
 Ala Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys
 305 310 315 320
 Lys Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr
 325 330 335
 Gly Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys
 340 345 350
 Ser His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val
 355 360 365
 Cys Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu
 370 375 380
 Cys Glu Ala Lys Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile
 385 390 395 400
 Ala Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys
 405 410 415
 Asp Ile Asn Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser
 420 425 430
 Cys Arg Asp Leu Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr
 435 440 445
 Ala Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro
 450 455 460
 Cys Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys
 465 470 475 480
 Leu Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp
 485 490 495
 Tyr Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg
 500 505 510
 Ala Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn
 515 520 525
 Cys Ser His Leu Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile
 530 535 540
 Asp Ser Cys Thr Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val
 545 550 555 560
 Arg Tyr Ile Ser Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser
 565 570 575

Gln Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly
 580 585 590
 Thr Tyr Cys His Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg
 595 600 605
 Asn Gly Gly Thr Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys
 610 615 620
 Ser Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys
 625 630 635 640
 Ser Gln Asn Pro Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn
 645 650 655
 Asp Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His
 660 665 670
 Ser Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr
 675 680 685
 Cys Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp
 690 695 700
 Glu Gly Thr Thr Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn
 705 710 715 720
 Pro Cys His Asn Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr
 725 730 735
 Cys Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr
 740 745 750
 Asn Asp Cys Ser Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp
 755 760 765
 Gly Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro
 770 775 780
 Asp Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe
 785 790 795 800
 Gly Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro
 805 810 815
 Pro Gly His Ser Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys
 820 825 830
 Ile Thr Met Gly Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp
 835 840 845
 Cys Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val
 850 855 860
 Trp Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys
 865 870 875 880

Pro Ser Gly Gln Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val
 885 890 895
 His Pro Cys Thr Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro
 900 905 910
 Val Lys Thr Lys Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala
 915 920 925
 Asn Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr
 930 935 940
 Thr Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn
 945 950 955 960
 Val Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser
 965 970 975
 Ala Asn Asn Glu Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp
 980 985 990
 Asp Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val
 995 1000 1005
 Ser Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val
 1010 1015 1020
 Arg Val Gln Arg Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro
 1025 1030 1035 1040
 Leu Leu Ser Ser Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr
 1045 1050 1055
 Ala Phe Tyr Trp Cys Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr
 1060 1065 1070
 His Ser Ala Ser Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu
 1075 1080 1085
 Asn Gln Ile Lys Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro
 1090 1095 1100
 Ile Lys Asp Tyr Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr
 1105 1110 1115 1120
 His Asn Ser Glu Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys
 1125 1130 1135
 Ala Arg Phe Ala Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu Glu
 1140 1145 1150
 Lys Pro Pro Asn Gly Thr Pro Thr Lys His Pro Asn Trp Thr Asn Lys
 1155 1160 1165
 Gln Asp Asn Arg Asp Leu Glu Ser Ala Gln Ser Leu Asn Arg Met Glu
 1170 1175 1180

Tyr Ile Val
1185

<210> 8
<211> 2663
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (179)..(2347)

<400> 8
cttgggaaga ggcggagacc ggcttttaaa gaaagaagtc ctgggtcctg cggctctgggg 60
cgaggcaagg gcgcttttct gcccacgctc cccgtggccc atcgatcccc cgcgcgtccg 120
ccgctgttct aaggagagaa gtggggggccc cccaggctcg cgcgtggagc gaagcagc 178
atg ggc agt cgg tgc gcg ctg gcc ctg gcg gtg ctc tcg gcc ttg ctg 226
Met Gly Ser Arg Cys Ala Leu Ala Leu Ala Val Leu Ser Ala Leu Leu
1 5 10 15
tgt cag gtc tgg agc tct ggg gtg ttc gaa ctg aag ctg cag gag ttc 274
Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe
20 25 30
gtc aac aag aag ggg ctg ctg ggg aac cgc aac tgc tgc cgc ggg ggc 322
Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly
35 40 45
gcg ggg cca ccg ccg tgc gcc tgc cgg acc ttc ttc cgc gtg tgc ctc 370
Ala Gly Pro Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu
50 55 60
aag cac tac cag gcc agc gtg tcc ccc gag ccg ccc tgc acc tac ggc 418
Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
65 70 75 80
agc gcc gtc acc ccc gtg ctg ggc gtc gac tcc ttc agt ctg ccc gac 466
Ser Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp
85 90 95
ggc ggg ggc gcc gac tcc gcg ttc agc aac ccc atc cgc ttc ccc ttc 514
Gly Gly Gly Ala Asp Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe
100 105 110
ggc ttc acc tgg ccg ggc acc ttc tct ctg att att gaa gct ctc cac 562
Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His
115 120 125
aca gat tct cct gat gac ctc gca aca gaa aac cca gaa aga ctc atc 610
Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile
130 135 140

agc	cgc	ctg	gcc	acc	cag	agg	cac	ctg	acg	gtg	ggc	gag	gag	tgg	tcc	658
Ser	Arg	Leu	Ala	Thr	Gln	Arg	His	Leu	Thr	Val	Gly	Glu	Glu	Trp	Ser	
145					150					155					160	
cag	gac	ctg	cac	agc	agc	ggc	cgc	acg	gac	ctc	aag	tac	tcc	tac	cgc	706
Gln	Asp	Leu	His	Ser	Ser	Gly	Arg	Thr	Asp	Leu	Lys	Tyr	Ser	Tyr	Arg	
				165					170						175	
ttc	gtg	tgt	gac	gaa	cac	tac	tac	gga	gag	ggc	tgc	tcc	gtt	ttc	tgc	754
Phe	Val	Cys	Asp	Glu	His	Tyr	Tyr	Gly	Glu	Gly	Cys	Ser	Val	Phe	Cys	
			180					185					190			
cgt	ccc	cgg	gac	gat	gcc	ttc	ggc	cac	ttc	acc	tgt	ggg	gag	cgt	ggg	802
Arg	Pro	Arg	Asp	Asp	Ala	Phe	Gly	His	Phe	Thr	Cys	Gly	Glu	Arg	Gly	
		195					200					205				
gag	aaa	gtg	tgc	aac	cct	ggc	tgg	aaa	ggg	ccc	tac	tgc	aca	gag	ccg	850
Glu	Lys	Val	Cys	Asn	Pro	Gly	Trp	Lys	Gly	Pro	Tyr	Cys	Thr	Glu	Pro	
	210					215				220						
atc	tgc	ctg	cct	gga	tgt	gat	gag	cag	cat	gga	ttt	tgt	gac	aaa	cca	898
Ile	Cys	Leu	Pro	Gly	Cys	Asp	Glu	Gln	His	Gly	Phe	Cys	Asp	Lys	Pro	
225					230					235					240	
ggg	gaa	tgc	aag	tgc	aga	gtg	ggc	tgg	cag	ggc	cgg	tac	tgt	gac	gag	946
Gly	Glu	Cys	Lys	Cys	Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu	
				245					250						255	
tgt	atc	cgc	tat	cca	ggc	tgt	ctc	cat	ggc	acc	tgc	cag	cag	ccc	tgg	994
Cys	Ile	Arg	Tyr	Pro	Gly	Cys	Leu	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp	
			260					265						270		
cag	tgc	aac	tgc	cag	gaa	ggc	tgg	ggg	ggc	ctt	ttc	tgc	aac	cag	gac	1042
Gln	Cys	Asn	Cys	Gln	Glu	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp	
		275					280					285				
ctg	aac	tac	tgc	aca	cac	cat	aag	ccc	tgc	aag	aat	gga	gcc	acc	tgc	1090
Leu	Asn	Tyr	Cys	Thr	His	His	Lys	Pro	Cys	Lys	Asn	Gly	Ala	Thr	Cys	
	290					295					300					
acc	aac	acg	ggc	cag	ggg	agc	tac	act	tgc	tct	tgc	cgg	cct	ggg	tac	1138
Thr	Asn	Thr	Gly	Gln	Gly	Ser	Tyr	Thr	Cys	Ser	Cys	Arg	Pro	Gly	Tyr	
305					310				315						320	
aca	ggt	gcc	acc	tgc	gag	ctg	ggg	att	gac	gag	tgt	gac	ccc	agc	cct	1186
Thr	Gly	Ala	Thr	Cys	Glu	Leu	Gly	Ile	Asp	Glu	Cys	Asp	Pro	Ser	Pro	
				325					330					335		
tgt	aag	aac	gga	ggg	agc	tgc	acg	gat	ctc	gag	aac	agc	tac	tcc	tgt	1234
Cys	Lys	Asn	Gly	Gly	Ser	Cys	Thr	Asp	Leu	Glu	Asn	Ser	Tyr	Ser	Cys	
			340					345						350		
acc	tgc	cca	ccc	ggc	ttc	tac	ggc	aaa	atc	tgt	gaa	ttg	agt	gcc	atg	1282
Thr	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Lys	Ile	Cys	Glu	Leu	Ser	Ala	Met	
		355					360					365				

acc	tgt	gcg	gac	ggc	cct	tgc	ttt	aac	ggg	ggt	cgg	tgc	tca	gac	agc	1330
Thr	Cys	Ala	Asp	Gly	Pro	Cys	Phe	Asn	Gly	Gly	Arg	Cys	Ser	Asp	Ser	
370						375					380					
ccc	gat	gga	ggg	tac	agc	tgc	cgc	tgc	ccc	gtg	ggc	tac	tcc	ggc	ttc	1378
Pro	Asp	Gly	Gly	Tyr	Ser	Cys	Arg	Cys	Pro	Val	Gly	Tyr	Ser	Gly	Phe	
385					390				395						400	
aac	tgt	gag	aag	aaa	att	gac	tac	tgc	agc	tct	tca	ccc	tgt	tct	aat	1426
Asn	Cys	Glu	Lys	Lys	Ile	Asp	Tyr	Cys	Ser	Ser	Ser	Pro	Cys	Ser	Asn	
				405					410						415	
ggt	gcc	aag	tgt	gtg	gac	ctc	ggt	gat	gcc	tac	ctg	tgc	cgc	tgc	cag	1474
Gly	Ala	Lys	Cys	Val	Asp	Leu	Gly	Asp	Ala	Tyr	Leu	Cys	Arg	Cys	Gln	
			420					425					430			
gcc	ggc	ttc	tgc	ggg	agg	cac	tgt	gac	gac	aac	gtg	gac	gac	tgc	gcc	1522
Ala	Gly	Phe	Ser	Gly	Arg	His	Cys	Asp	Asp	Asn	Val	Asp	Asp	Cys	Ala	
		435					440					445				
tcc	tcc	ccg	tgc	gcc	aac	ggg	ggc	acc	tgc	cgg	gat	ggc	gtg	aac	gac	1570
Ser	Ser	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	Arg	Asp	Gly	Val	Asn	Asp	
	450					455					460					
ttc	tcc	tgc	acc	tgc	ccg	cct	ggc	tac	acg	ggc	agg	aac	tgc	agt	gcc	1618
Phe	Ser	Cys	Thr	Cys	Pro	Pro	Gly	Tyr	Thr	Gly	Arg	Asn	Cys	Ser	Ala	
465					470					475					480	
ccc	gtc	agc	agg	tgc	gag	cac	gca	ccc	tgc	cac	aat	ggg	gcc	acc	tgc	1666
Pro	Val	Ser	Arg	Cys	Glu	His	Ala	Pro	Cys	His	Asn	Gly	Ala	Thr	Cys	
				485					490					495		
cac	gag	agg	ggc	cac	cgc	tat	gtg	tgc	gag	tgt	gcc	cga	ggc	tac	ggg	1714
His	Glu	Arg	Gly	His	Arg	Tyr	Val	Cys	Glu	Cys	Ala	Arg	Gly	Tyr	Gly	
			500					505					510			
ggt	ccc	aac	tgc	cag	ttc	ctg	ctc	ccc	gag	ctg	ccc	ccg	ggc	cca	gcg	1762
Gly	Pro	Asn	Cys	Gln	Phe	Leu	Leu	Pro	Glu	Leu	Pro	Pro	Gly	Pro	Ala	
		515				520						525				
gtg	gtg	gac	ctc	act	gag	aag	cta	gag	ggc	cag	ggc	ggg	cca	ttc	ccc	1810
Val	Val	Asp	Leu	Thr	Glu	Lys	Leu	Glu	Gly	Gln	Gly	Gly	Pro	Phe	Pro	
		530				535					540					
tgg	gtg	gcc	gtg	tgc	gcc	ggg	gtc	atc	ctt	gtc	ctc	atg	ctg	ctg	ctg	1858
Trp	Val	Ala	Val	Cys	Ala	Gly	Val	Ile	Leu	Val	Leu	Met	Leu	Leu	Leu	
545					550					555					560	
ggc	tgt	gcc	gct	gtg	gtg	gtc	tgc	gtc	cgg	ctg	agg	ctg	cag	aag	cac	1906
Gly	Cys	Ala	Ala	Val	Val	Val	Cys	Val	Arg	Leu	Arg	Leu	Gln	Lys	His	
				565					570					575		
cgg	ccc	cca	gcc	gac	ccc	tgc	cgg	ggg	gag	acg	gag	acc	atg	aac	aac	1954
Arg	Pro	Pro	Ala	Asp	Pro	Cys	Arg	Gly	Glu	Thr	Glu	Thr	Met	Asn	Asn	
			580					585					590			

ctg gcc aac tgc cag cgt gag aag gac atc tca gtc agc atc atc ggg 2002
Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly
595 600 605

```
gcc acg cag atc aag aac acc aac aag aag gcg gac ttc cac ggg gac      2050
Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp
      610                      615                      620
```

cac agc gcc gac aag aat ggc ttc aag gcc cgc tac cca gcg gtg gac 2098
 His Ser Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro Ala Val Asp
 625 630 635 640

tat	aac	ctc	gtg	cag	gac	ctc	aag	ggg	gac	gac	acc	gcc	gtc	agg	gac	2146
Tyr	Asn	Leu	Val	Gln	Asp	Leu	Lys	Gly	Asp	Asp	Thr	Ala	Val	Arg	Asp	
				645					650					655		

gcg cac agc aag cgt gac acc aag tgc cag ccc cag ggc tcc tca ggg 2194
Ala His Ser Lys Arg Asp Thr Lys Cys Gln Pro Gln Gly Ser Ser Gly
660 665 670

gag gag aag ggg acc ccg acc aca ctc agg ggt gga gaa gca tct gaa 2242
Glu Glu Lys Gly Thr Pro Thr Thr Leu Arg Gly Gly Glu Ala Ser Glu
675 680 685

aga aaa agg ccg gac tcg ggc tgt tca act tca aaa gac acc aag tac 2290
Arg Lys Arg Pro Asp Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr
690 695 700

cag	tcg	gtg	tac	gtc	ata	tcc	gag	gag	aag	gat	gag	tgc	gtc	ata	gca	2338
Gln	Ser	Val	Tyr	Val	Ile	Ser	Glu	Glu	Lys	Asp	Glu	Cys	Val	Ile	Ala	
705					710					715					720	

act gag gtg taaaatggaa gtgagatggc aagactcccg tttctcttaa 2387
Thr Glu Val

aataagtaaa attccaagga tatatgcccc aacgaatgct gctgaagaag agggagqcct 2447

cgtggactgc tgctgagaaa ccgagttcag accgagcagg ttctcctcct gaggtcctcg 2507

acgcctgccg acagcctgtc gcggcccggc cgcttgcggc actgccttcc gtgacgtcgc 2567

cgttgcaacta tggacagttg ctcttaagag aatatatatt taaatgggtg aactgaatta 2627

cgcataagaa gcatgcactg cctgagtgta tatattt 2663

<210> 9

<211> 723

<212> PRT

<213> Homo sapiens

<400> 9

Met Gly Ser Arg Cys Ala Leu Ala Leu Ala Val Leu Ser Ala Leu Leu
1 5 10 15

Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe
20 25 30

Val	Asn	Lys	Lys	Gly	Leu	Leu	Gly	Asn	Arg	Asn	Cys	Cys	Arg	Gly	Gly
		35					40					45			
Ala	Gly	Pro	Pro	Pro	Cys	Ala	Cys	Arg	Thr	Phe	Phe	Arg	Val	Cys	Leu
		50				55					60				
Lys	His	Tyr	Gln	Ala	Ser	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr	Tyr	Gly
		65			70					75					80
Ser	Ala	Val	Thr	Pro	Val	Leu	Gly	Val	Asp	Ser	Phe	Ser	Leu	Pro	Asp
				85					90					95	
Gly	Gly	Gly	Ala	Asp	Ser	Ala	Phe	Ser	Asn	Pro	Ile	Arg	Phe	Pro	Phe
			100					105					110		
Gly	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Leu	His
		115					120					125			
Thr	Asp	Ser	Pro	Asp	Asp	Leu	Ala	Thr	Glu	Asn	Pro	Glu	Arg	Leu	Ile
		130				135					140				
Ser	Arg	Leu	Ala	Thr	Gln	Arg	His	Leu	Thr	Val	Gly	Glu	Glu	Trp	Ser
		145			150					155					160
Gln	Asp	Leu	His	Ser	Ser	Gly	Arg	Thr	Asp	Leu	Lys	Tyr	Ser	Tyr	Arg
				165					170					175	
Phe	Val	Cys	Asp	Glu	His	Tyr	Tyr	Gly	Glu	Gly	Cys	Ser	Val	Phe	Cys
			180					185					190		
Arg	Pro	Arg	Asp	Asp	Ala	Phe	Gly	His	Phe	Thr	Cys	Gly	Glu	Arg	Gly
		195					200					205			
Glu	Lys	Val	Cys	Asn	Pro	Gly	Trp	Lys	Gly	Pro	Tyr	Cys	Thr	Glu	Pro
		210				215					220				
Ile	Cys	Leu	Pro	Gly	Cys	Asp	Glu	Gln	His	Gly	Phe	Cys	Asp	Lys	Pro
		225			230					235					240
Gly	Glu	Cys	Lys	Cys	Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu
				245					250					255	
Cys	Ile	Arg	Tyr	Pro	Gly	Cys	Leu	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp
			260					265					270		
Gln	Cys	Asn	Cys	Gln	Glu	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp
		275				280					285				
Leu	Asn	Tyr	Cys	Thr	His	His	Lys	Pro	Cys	Lys	Asn	Gly	Ala	Thr	Cys
		290				295					300				
Thr	Asn	Thr	Gly	Gln	Gly	Ser	Tyr	Thr	Cys	Ser	Cys	Arg	Pro	Gly	Tyr
		305			310					315					320
Thr	Gly	Ala	Thr	Cys	Glu	Leu	Gly	Ile	Asp	Glu	Cys	Asp	Pro	Ser	Pro
				325					330					335	

Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys
 340 345 350
 Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met
 355 360 365
 Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser
 370 375 380
 Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe
 385 390 395 400
 Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn
 405 410 415
 Gly Ala Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln
 420 425 430
 Ala Gly Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala
 435 440 445
 Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp
 450 455 460
 Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala
 465 470 475 480
 Pro Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys
 485 490 495
 His Glu Arg Gly His Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly
 500 505 510
 Gly Pro Asn Cys Gln Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala
 515 520 525
 Val Val Asp Leu Thr Glu Lys Leu Glu Gly Gln Gly Gly Pro Phe Pro
 530 535 540
 Trp Val Ala Val Cys Ala Gly Val Ile Leu Val Leu Met Leu Leu Leu
 545 550 555 560
 Gly Cys Ala Ala Val Val Val Cys Val Arg Leu Arg Leu Gln Lys His
 565 570 575
 Arg Pro Pro Ala Asp Pro Cys Arg Gly Glu Thr Glu Thr Met Asn Asn
 580 585 590
 Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly
 595 600 605
 Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp
 610 615 620
 His Ser Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro Ala Val Asp
 625 630 635 640

[illegible]

```
<210> 10
<211> 4208
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (409) .. (4062)
```

```

<400> 10
ggccggcccg cgagctaggc tggttttttt ttttctcccc tccctccccc ctttttccat 60
gcagctgata taaaagggaa taaaaggctg cgcataatca taataataaa agaaggggag 120
cgcgagagaa ggaaagaaa cggggaggtg gaagaggagg gggagcgtct caaagaagcg 180
atcagaataa taaaaggagg ccgggctctt tgccttctgg aacgggccgc tcttgaaagg 240
gcttttgaaa agtggtgttg ttttccagtc gtgcatgctc caatcggcgg agtatattag 300
agccgggacg cggcggccgc aggggcagcg gcgacggcag caccggcggc agcaccagcg 360
cgaacagcag cggcggcgtc ccgagtgccg gcggcgcgcg gcgcagcg atg cgt tcc 417
                               Met Arg Ser
                               1

```

cca	cgg	acg	cgc	ggc	cgg	tcc	ggg	cgc	ccc	cta	agc	ctc	ctg	ctc	gcc	465
Pro	Arg	Thr	Arg	Gly	Arg	Ser	Gly	Arg	Pro	Leu	Ser	Leu	Leu	Leu	Ala	
	5					10					15					
ctg	ctc	tgt	gcc	ctg	cga	gcc	aag	gtg	tgt	ggg	gcc	tcg	ggt	cag	ttc	513
Leu	Leu	Cys	Ala	Leu	Arg	Ala	Lys	Val	Cys	Gly	Ala	Ser	Gly	Gln	Phe	
	20				25					30					35	
gag	ttg	gag	atc	ctg	tcc	atg	cag	aac	gtg	aac	ggg	gag	ctg	cag	aac	561
Glu	Leu	Glu	Ile	Leu	Ser	Met	Gln	Asn	Val	Asn	Gly	Glu	Leu	Gln	Asn	
				40					45					50		

ggg aac tgc tgc ggc ggc gcc cgg aac ccg gga gac cgc aag tgc acc Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg Lys Cys Thr 55 60 65	609
cgc gac gag tgt gac aca tac ttc aaa gtg tgc ctc aag gag tat cag Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys Glu Tyr Gln 70 75 80	657
tcc cgc gtc acg gcc ggg ggg ccc tgc agc ttc ggc tca ggg tcc acg Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser Gly Ser Thr 85 90 95	705
cct gtc atc ggg ggc aac acc ttc aac ctc aag gcc agc cgc ggc aac Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser Arg Gly Asn 100 105 110 115	753
gac cgc aac cgc atc gtg ctg cct ttc agt ttc gcc tgg ccg agg tcc Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp Pro Arg Ser 120 125 130	801
tat acg ttg ctt gtg gag gcg tgg gat tcc agt aat gac acc gtt caa Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp Thr Val Gln 135 140 145	849
cct gac agt att att gaa aag gct tct cac tcg ggc atg atc aac ccc Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met Ile Asn Pro 150 155 160	897
agc cgg cag tgg cag acg ctg aag cag aac acg ggc gtt gcc cac ttt Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val Ala His Phe 165 170 175	945
gag tat cag atc cgc gtg acc tgt gat gac tac tac tat ggc ttt ggc Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr Gly Phe Gly 180 185 190 195	993
tgc aat aag ttc tgc cgc ccc aga gat gac ttc ttt gga cac tat gcc Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala 200 205 210	1041
tgt gac cag aat ggc aac aaa act tgc atg gaa ggc tgg atg ggc ccc Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro 215 220 225	1089
gaa tgt aac aga gct att tgc cga caa ggc tgc agt cct aag cat ggg Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro Lys His Gly 230 235 240	1137
tct tgc aaa ctc cca ggt gac tgc agg tgc cag tac ggc tgg caa ggc Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly Trp Gln Gly 245 250 255	1185
ctg tac tgt gat aag tgc atc cca cac ccg gga tgc gtc cac ggc atc Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val His Gly Ile 260 265 270 275	1233

tgt aat gag ccc tgg cag tgc ctc tgt gag acc aac tgg ggc ggc cag	1281
Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp Gly Gly Gln	
280 285 290	
ctc tgt gac aaa gat ctc aat tac tgt ggg act cat cag ccg tgt ctc	1329
Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln Pro Cys Leu	
295 300 305	
aac ggg gga act tgt agc aac aca ggc cct gac aaa tat cag tgt tcc	1377
Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr Gln Cys Ser	
310 315 320	
tgc cct gag ggg tat tca gga ccc aac tgt gaa att gct gag cac gcc	1425
Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala Glu His Ala	
325 330 335	
tgc ctc tct gat ccc tgt cac aac aga ggc agc tgt aag gag acc tcc	1473
Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys Glu Thr Ser	
340 345 350 355	
ctg ggc ttt gag tgt gag tgt tcc cca ggc tgg acc ggc ccc aca tgc	1521
Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly Pro Thr Cys	
360 365 370	
tct aca aac att gat gac tgt tct cct aat aac tgt tcc cac ggg ggc	1569
Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser His Gly Gly	
375 380 385	
acc tgc cag gac ctg gtt aac gga ttt aag tgt gtg tgc ccc cca cag	1617
Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys Pro Pro Gln	
390 395 400	
tgg act ggg aaa acg tgc cag tta gat gca aat gaa tgt gag gcc aaa	1665
Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys Glu Ala Lys	
405 410 415	
cct tgt gta aac gcc aaa tcc tgt aag aat ctc att gcc agc tac tac	1713
Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala Ser Tyr Tyr	
420 425 430 435	
tgc gac tgt ctt ccc ggc tgg atg ggt cag aat tgt gac ata aat att	1761
Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp Ile Asn Ile	
440 445 450	
aat gac tgc ctt ggc cag tgt cag aat gac gcc tcc tgt cgg gat ttg	1809
Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys Arg Asp Leu	
455 460 465	
gtt aat ggt tat cgc tgt atc tgt cca cct ggc tat gca ggc gat cac	1857
Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala Gly Asp His	
470 475 480	
tgt gag aga gac atc gat gaa tgt gcc agc aac ccc tgt ttg aat ggg	1905
Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys Leu Asn Gly	
485 490 495	

ggt cac tgt cag aat gaa atc aac aga ttc cag tgt ctg tgt ccc act	1953
Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu Cys Pro Thr	
500 505 510 515	
ggt ttc tct gga aac ctc tgt cag ctg gac atc gat tat tgt gag cct	2001
Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr Cys Glu Pro	
520 525 530	
aat ccc tgc cag aac ggt gcc cag tgc tac aac cgt gcc agt gac tat	2049
Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala Ser Asp Tyr	
535 540 545	
ttc tgc aag tgc ccc gag gac tat gag ggc aag aac tgc tca cac ctg	2097
Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys Ser His Leu	
550 555 560	
aaa gac cac tgc cgc acg acc ccc tgt gaa gtg att gac agc tgc aca	2145
Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile Asp Ser Cys Thr	
565 570 575	
gtg gcc atg gct tcc aac gac aca cct gaa ggg gtg cgg tat att tcc	2193
Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val Arg Tyr Ile Ser	
580 585 590 595	
tcc aac gtc tgt ggt cct cac ggg aag tgc aag agt cag tcg gga ggc	2241
Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser Gln Ser Gly Gly	
600 605 610	
aaa ttc acc tgt gac tgt aac aaa ggc ttc acg gga aca tac tgc cat	2289
Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr Tyr Cys His	
615 620 625	
gaa aat att aat gac tgt gag agc aac cct tgt aga aac ggt ggc act	2337
Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn Gly Gly Thr	
630 635 640	
tgc atc gat ggt gtc aac tcc tac aag tgc atc tgt agt gac ggc tgg	2385
Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser Asp Gly Trp	
645 650 655	
gag ggg gcc tac tgt gaa acc aat att aat gac tgc agc cag aac ccc	2433
Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser Gln Asn Pro	
660 665 670 675	
tgc cac aat ggg ggc acg tgt cgc gac ctg gtc aat gac ttc tac tgt	2481
Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn Asp Phe Tyr Cys	
680 685 690	
gac tgt aaa aat ggg tgg aaa gga aag acc tgc cac tca cgt gac agt	2529
Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His Ser Arg Asp Ser	
695 700 705	
cag tgt gat gag gcc acg tgc aac aac ggt ggc acc tgc tat gat gag	2577
Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys Tyr Asp Glu	
710 715 720	

ggg gat gct ttt aag tgc atg tgt cct ggc ggc tgg gaa gga aca acc Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp Glu Gly Thr Thr 725 730 735	2625
tgt aac ata gcc cga aac agt agc tgc ctg ccc aac ccc tgc cat aat Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn Pro Cys His Asn 740 745 750 755	2673
ggg ggc aca tgt gtg gtc aac ggc gag tcc ttt acg tgc gtc tgc aag Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr Cys Val Cys Lys 760 765 770	2721
gaa ggc tgg gag ggg ccc atc tgt gct cag aat acc aat gac tgc agc Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr Asn Asp Cys Ser 775 780 785	2769
cct cat ccc tgt tac aac agc ggc acc tgt gtg gat gga gac aac tgg Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly Asp Asn Trp 790 795 800	2817
tac cgg tgc gaa tgt gcc ccg ggt ttt gct ggg ccc gac tgc aga ata Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp Cys Arg Ile 805 810 815	2865
aac atc aat gaa tgc cag tct tca cct tgt gcc ttt gga gcg acc tgt Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly Ala Thr Cys 820 825 830 835	2913
gtg gat gag atc aat ggc tac cgg tgt gtc tgc cct cca ggg cac agt Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro Gly His Ser 840 845 850	2961
ggt gcc aag tgc cag gaa gtt tca ggg aga cct tgc atc acc atg ggg Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys Ile Thr Met Gly 855 860 865	3009
agt gtg ata cca gat ggg gcc aaa tgg gat gat gac tgt aat acc tgc Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp Cys Asn Thr Cys 870 875 880	3057
cag tgc ctg aat gga cgg atc gcc tgc tca aag gtc tgg tgt ggc cct Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val Trp Cys Gly Pro 885 890 895	3105
cga cct tgc ctg ctc cac aaa ggg cac agc gag tgc ccc agc ggg cag Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys Pro Ser Gly Gln 900 905 910 915	3153
agc tgc atc ccc atc ctg gac gac cag tgc ttc gtc cac ccc tgc act Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His Pro Cys Thr 920 925 930	3201
ggt gtg ggc gag tgt cgg tct tcc agt ctc cag ccg gtg aag aca aag Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val Lys Thr Lys 935 940 945	3249

tgc acc tct gac tcc tat tac cag gat aac tgt gcg aac atc aca ttt Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn Ile Thr Phe 950 955 960	3297
acc ttt aac aag gag atg atg tca cca ggt ctt act acg gag cac att Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr Glu His Ile 965 970 975	3345
tgc agt gaa ttg agg aat ttg aat att ttg aag aat gtt tcc gct gaa Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val Ser Ala Glu 980 985 990 995	3393
tat tca atc tac atc gct tgc gag cct tcc cct tca gcg aac aat gaa Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala Asn Asn Glu 1000 1005 1010	3441
ata cat gtg gcc att tct gct gaa gat ata cgg gat gat ggg aac ccg Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp Gly Asn Pro 1015 1020 1025	3489
atc aag gaa atc act gac aaa ata atc gat ctt gtt agt aaa cgt gat Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser Lys Arg Asp 1030 1035 1040	3537
gga aac agc tcg ctg att gct gcc gtt gca gaa gta aga gtt cag agg Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg Val Gln Arg 1045 1050 1055	3585
cgg cct ctg aag aac aga aca gat ttc ctt gtt ccc ttg ctg agc tct Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu Leu Ser Ser 1060 1065 1070 1075	3633
gtc tta act gtg gct tgg atc tgt tgc ttg gtg acg gcc ttc tac tgg Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp 1080 1085 1090	3681
tgc ctg cgg aag cgg cgg aag ccg ggc agc cac aca cac tca gcc tct Cys Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr His Ser Ala Ser 1095 1100 1105	3729
gag gac aac acc acc aac aac gtg cgg gag cag ctg aac cag atc aaa Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu Asn Gln Ile Lys 1110 1115 1120	3777
aac ccc att gag aaa cat ggg gcc aac acg gtc ccc atc aag gat tat Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile Lys Asp Tyr 1125 1130 1135	3825
gag aac aag aac tcc aaa atg tct aaa ata agg aca cac aat tct gaa Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His Asn Ser Glu 1140 1145 1150 1155	3873
gta gaa gag gac gac atg gac aaa cac cag cag aaa gcc cgg ttt gcc Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys Ala Arg Phe Ala 1160 1165 1170	3921

aag cag ccg gcg tac acg ctg gta gac aga gaa gag aag ccc ccc aac 3969
 Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu Glu Lys Pro Pro Asn
 1175 1180 1185

ggc acg ccg aca aaa cac cca aac tgg aca aac aaa cag gac aac aga 4017
 Gly Thr Pro Thr Lys His Pro Asn Trp Thr Asn Lys Gln Asp Asn Arg
 1190 1195 1200

gac ttg gaa agt gcc cag agc tta aac cga atg gag tac atc gta 4062
 Asp Leu Glu Ser Ala Gln Ser Leu Asn Arg Met Glu Tyr Ile Val
 1205 1210 1215

tagcagaccg cgggcactgc cgccgctagg tagagtctga gggctttagg ttctttaaac 4122

tgctgtgtca tactcgagtc tgaggccggt gctgacttag aatccctgtg ttaatttaag 4182

ttttgacaag ctggcttaca ctggca 4208

<210> 11

<211> 1218

<212> PRT

<213> Homo sapiens

<400> 11

Met Arg Ser Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu
 1 5 10 15

Leu Leu Ala Leu Leu Cys Ala Leu Arg Ala Lys Val Cys Gly Ala Ser
 20 25 30

Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu
 35 40 45

Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg
 50 55 60

Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys
 65 70 75 80

Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser
 85 90 95

Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser
 100 105 110

Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp
 115 120 125

Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp
 130 135 140

Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met
 145 150 155 160

Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
 165 170 175

Ala	His	Phe	Glu	Tyr	Gln	Ile	Arg	Val	Thr	Cys	Asp	Asp	Tyr	Tyr	Tyr	180	185	190
Gly	Phe	Gly	Cys	Asn	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Phe	Phe	Gly	195	200	205
His	Tyr	Ala	Cys	Asp	Gln	Asn	Gly	Asn	Lys	Thr	Cys	Met	Glu	Gly	Trp	210	215	220
Met	Gly	Pro	Glu	Cys	Asn	Arg	Ala	Ile	Cys	Arg	Gln	Gly	Cys	Ser	Pro	225	230	235
Lys	His	Gly	Ser	Cys	Lys	Leu	Pro	Gly	Asp	Cys	Arg	Cys	Gln	Tyr	Gly	245	250	255
Trp	Gln	Gly	Leu	Tyr	Cys	Asp	Lys	Cys	Ile	Pro	His	Pro	Gly	Cys	Val	260	265	270
His	Gly	Ile	Cys	Asn	Glu	Pro	Trp	Gln	Cys	Leu	Cys	Glu	Thr	Asn	Trp	275	280	285
Gly	Gly	Gln	Leu	Cys	Asp	Lys	Asp	Leu	Asn	Tyr	Cys	Gly	Thr	His	Gln	290	295	300
Pro	Cys	Leu	Asn	Gly	Gly	Thr	Cys	Ser	Asn	Thr	Gly	Pro	Asp	Lys	Tyr	305	310	315
Gln	Cys	Ser	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	Pro	Asn	Cys	Glu	Ile	Ala	325	330	335
Glu	His	Ala	Cys	Leu	Ser	Asp	Pro	Cys	His	Asn	Arg	Gly	Ser	Cys	Lys	340	345	350
Glu	Thr	Ser	Leu	Gly	Phe	Glu	Cys	Glu	Cys	Ser	Pro	Gly	Trp	Thr	Gly	355	360	365
Pro	Thr	Cys	Ser	Thr	Asn	Ile	Asp	Asp	Cys	Ser	Pro	Asn	Asn	Cys	Ser	370	375	380
His	Gly	Gly	Thr	Cys	Gln	Asp	Leu	Val	Asn	Gly	Phe	Lys	Cys	Val	Cys	385	390	395
Pro	Pro	Gln	Trp	Thr	Gly	Lys	Thr	Cys	Gln	Leu	Asp	Ala	Asn	Glu	Cys	405	410	415
Glu	Ala	Lys	Pro	Cys	Val	Asn	Ala	Lys	Ser	Cys	Lys	Asn	Leu	Ile	Ala	420	425	430
Ser	Tyr	Tyr	Cys	Asp	Cys	Leu	Pro	Gly	Trp	Met	Gly	Gln	Asn	Cys	Asp	435	440	445
Ile	Asn	Ile	Asn	Asp	Cys	Leu	Gly	Gln	Cys	Gln	Asn	Asp	Ala	Ser	Cys	450	455	460
Arg	Asp	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Ile	Cys	Pro	Pro	Gly	Tyr	Ala	465	470	475
																		480

Gly	Asp	His	Cys	Glu	Arg	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Asn	Pro	Cys	
				485					490					495		
Leu	Asn	Gly	Gly	His	Cys	Gln	Asn	Glu	Ile	Asn	Arg	Phe	Gln	Cys	Leu	
			500					505					510			
Cys	Pro	Thr	Gly	Phe	Ser	Gly	Asn	Leu	Cys	Gln	Leu	Asp	Ile	Asp	Tyr	
		515					520					525				
Cys	Glu	Pro	Asn	Pro	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Tyr	Asn	Arg	Ala	
	530					535					540					
Ser	Asp	Tyr	Phe	Cys	Lys	Cys	Pro	Glu	Asp	Tyr	Glu	Gly	Lys	Asn	Cys	
545					550					555					560	
Ser	His	Leu	Lys	Asp	His	Cys	Arg	Thr	Thr	Pro	Cys	Glu	Val	Ile	Asp	
				565					570					575		
Ser	Cys	Thr	Val	Ala	Met	Ala	Ser	Asn	Asp	Thr	Pro	Glu	Gly	Val	Arg	
			580					585					590			
Tyr	Ile	Ser	Ser	Asn	Val	Cys	Gly	Pro	His	Gly	Lys	Cys	Lys	Ser	Gln	
		595					600					605				
Ser	Gly	Gly	Lys	Phe	Thr	Cys	Asp	Cys	Asn	Lys	Gly	Phe	Thr	Gly	Thr	
	610					615					620					
Tyr	Cys	His	Glu	Asn	Ile	Asn	Asp	Cys	Glu	Ser	Asn	Pro	Cys	Arg	Asn	
625					630					635					640	
Gly	Gly	Thr	Cys	Ile	Asp	Gly	Val	Asn	Ser	Tyr	Lys	Cys	Ile	Cys	Ser	
				645					650					655		
Asp	Gly	Trp	Glu	Gly	Ala	Tyr	Cys	Glu	Thr	Asn	Ile	Asn	Asp	Cys	Ser	
			660					665					670			
Gln	Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Arg	Asp	Leu	Val	Asn	Asp	
		675					680					685				
Phe	Tyr	Cys	Asp	Cys	Lys	Asn	Gly	Trp	Lys	Gly	Lys	Thr	Cys	His	Ser	
	690					695					700					
Arg	Asp	Ser	Gln	Cys	Asp	Glu	Ala	Thr	Cys	Asn	Asn	Gly	Gly	Thr	Cys	
705					710					715					720	
Tyr	Asp	Glu	Gly	Asp	Ala	Phe	Lys	Cys	Met	Cys	Pro	Gly	Gly	Trp	Glu	
				725					730					735		
Gly	Thr	Thr	Cys	Asn	Ile	Ala	Arg	Asn	Ser	Ser	Cys	Leu	Pro	Asn	Pro	
			740					745					750			
Cys	His	Asn	Gly	Gly	Thr	Cys	Val	Val	Asn	Gly	Glu	Ser	Phe	Thr	Cys	
		755					760					765				
Val	Cys	Lys	Glu	Gly	Trp	Glu	Gly	Pro	Ile	Cys	Ala	Gln	Asn	Thr	Asn	
	770					775					780					

Asp Cys Ser Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly
 785 790 795 800
 Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp
 805 810 815
 Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly
 820 825 830
 Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro
 835 840 845
 Gly His Ser Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys Ile
 850 855 860
 Thr Met Gly Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp Cys
 865 870 875 880
 Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val Trp
 885 890 895
 Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys Pro
 900 905 910
 Ser Gly Gln Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His
 915 920 925
 Pro Cys Thr Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val
 930 935 940
 Lys Thr Lys Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn
 945 950 955 960
 Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr
 965 970 975
 Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val
 980 985 990
 Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala
 995 1000 1005
 Asn Asn Glu Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp
 1010 1015 1020
 Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser
 1025 1030 1035 1040
 Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg
 1045 1050 1055
 Val Gln Arg Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu
 1060 1065 1070
 Leu Ser Ser Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala
 1075 1080 1085

Phe Tyr Trp Cys Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr His
 1090 1095 1100
 Ser Ala Ser Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu Asn
 1105 1110 1115 1120
 Gln Ile Lys Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile
 1125 1130 1135
 Lys Asp Tyr Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His
 1140 1145 1150
 Asn Ser Glu Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys Ala
 1155 1160 1165
 Arg Phe Ala Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu Glu Lys
 1170 1175 1180
 Pro Pro Asn Gly Thr Pro Thr Lys His Pro Asn Trp Thr Asn Lys Gln
 1185 1190 1195 1200
 Asp Asn Arg Asp Leu Glu Ser Ala Gln Ser Leu Asn Arg Met Glu Tyr
 1205 1210 1215
 Ile Val

<210> 12
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide

<220>
 <221> CDS
 <222> (1)..(24)

<400> 12
 gat tat aaa gat gat gat gat aaa tga
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

27

<210> 13
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 13
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 14
 tggcartgya aytgycarga 20

<210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 15
 atytttyt ccarttraa 20

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (12)
 <223> a, t, c, g, other or unknown

<400> 16
 tgcststgyg anaccaactg 20

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17
 tttatktcrc awktckgwcc 20

<210> 18
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

tcgcgcgtgg agcgaagcag catgg

25

<210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

ggaattcgat atcaagctta tcgat

25

<210> 20
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

tcacccgccc tggccctcta gcttctca

28

<210> 21
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

ggacgcgtgg atccactagt tctagagc

28

<210> 22
 <211> 55
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 22

tcatttatca tcatcatctt tataatcccc gccctggccc tctagcttct cagtg 55

<210> 23
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 aaccatcccc gaggggtgtct gctggaagcc aggctca 37

<210> 24
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 24
 cctctagagt cgcggccgtc gcaactcattt acc 33

<210> 25
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 25
 aaggatcccc gccctggccc tctagcttc 29

<210> 26
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 26
 cctctagacg cgtagagcgg ccgccaccgc ggtgga 36

<210> 27
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 27
 tcacacctca gttgctatga cgcac 25

<210> 28
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 28
 ggacgcgtgg atccactagt tctagagc 28

<210> 29
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 29
 tcatttatca tcatcatctt tataatccac ctcagttgct atgacgcact c 51

<210> 30
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 30
 cggcgacgcg atgcgttccc cacgg 25

<210> 31
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 31
 ggaattcgat atcaagctta tcgat 25

<210> 32
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
tcaatctgtt ctgttggtca gaggcgg 27

<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ggacgcgtgg atccactagt tctagagc 28

<210> 34
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
tcatttatca tcatcatctt tataatcatc tggttctgtg ttcagaggcc g 51

<210> 35
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
aaggatccgt tctgttggtc agaggccgcc t 31

<210> 36
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
cctctagacg cgtagagcgg ccgccaccgc ggtgga 36

<210> 37
<211> 28

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 37
 ctatacgatg tactccattc ggtttaag

28

<210> 38
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 38
 ggacgcgtct agagtcgacc tgcaggcatg c

31

<210> 39
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 39
 ctatttatca tcatcatott tataatctac gatgtactcc attcggttta ag

52

<210> 40
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)..(2)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (4)..(6)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (9)..(11)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (13)..(15)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (22)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (26)..(27)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (29)..(31)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (33)..(35)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (37)..(38)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (41)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (43)..(44)
 <223> Variable amino acid

<400> 40
 Xaa Xaa Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
 1 5 10 15

Arg Pro Arg Asp Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly
 20 25 30

Xaa Xaa Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys
 35 40 45

<210> 41
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 41

Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
 20 25 30

Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys
 35 40 45

<210> 42

<211> 45

<212> PRT

<213> Drosophila sp.

<400> 42

Val Thr Cys Asp Leu Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly
 20 25 30

Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp Tyr Cys
 35 40 45

<210> 43

<211> 45

<212> PRT

<213> Xenopus laevis

<400> 43

Phe Val Cys Asp Glu Tyr Tyr Tyr Gly Glu Gly Cys Ser Asp Tyr Cys
 1 5 10 15

Arg Pro Arg Asp Asp Ala Phe Gly His Phe Ser Cys Gly Glu Arg Gly
 20 25 30

Glu Lys Leu Cys Asn Pro Gly Trp Lys Gly Leu Tyr Cys
 35 40 45

<210> 44

<211> 45

<212> PRT

<213> Gallus sp.

<400> 44

Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg Gly
 20 25 30

Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Gln Tyr Cys
 35 40 45

<210> 45
 <211> 45
 <212> PRT
 <213> Murine sp.

<400> 45
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Asp Arg Gly
 20 25 30
 Glu Lys Met Cys Asp Pro Gly Trp Lys Gly Gln Tyr Cys
 35 40 45

<210> 46
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 46
 Val Thr Cys Asp Asp Tyr Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
 20 25 30
 Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro Glu Cys
 35 40 45

<210> 47
 <211> 45
 <212> PRT
 <213> Drosophila sp.

<400> 47
 Val Gln Cys Ala Val Thr Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Gln Phe Gly His Tyr Ala Cys Gly Ser Glu Gly
 20 25 30
 Gln Lys Leu Cys Leu Asn Gly Trp Gln Gly Val Asn Cys
 35 40 45

<210> 48
 <211> 45
 <212> PRT
 <213> Rattus sp.

<400> 48
 Val Thr Cys Asp Asp His Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
20 25 30

Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro Glu Cys
35 40 45